The Use of Lunasin Peptide as a Transcriptional Activator to Prevent Cancer and Related Methods for Treatment, Monitoring and Prognosis

[01] This application claims priority from the following United States Provisional Applications: 60/549,487, filed 1st March 2004, and 60/621,217, filed 21st October 2004. The invention was made in part with government support under Grant No. P60MD00222 awarded by the National Institutes of Health (NIH).

FIELD OF THE INVENTION

[02] The invention relates gene expression profiles produced in response to lunasin exposure, wherein such gene expression profiles correlate with anti-neoplastic activity.

BACKGROUND OF THE INVENTION

[03] Dietary factors play an important role in the etiology of different kinds of cancer (Greenwald et al., 2001). For example, soybean-rich diets are associated with lower cancer mortality rates, particularly for cancers of the colon, breast and prostate (Messina et al., 1994). Isoflavones and the Bowman-Birk protease inhibitor (BBI) are some of the many components in soybean believed to be responsible for suppressing carcinogenesis (Kennedy, 1995). Recently, lunasin, a small peptide found in soybean seeds, has shown promise as a agent that reduces the neoplastic effects of certain carcinogenic chemicals (a "anti-neoplastic" agent) (Galvez et al., 2001).

[04] Lunasin is a 43 amino acid small subunit of a soybean 2S albumin. The polynucleotide encoding the lunasin peptide, and the peptide sequence of lunasin are known and disclosed in U.S. patent No. 6,544,956 (hereby incorporated by reference in its entirety) in which the lunasin peptide is encoded by bases 80-208 of SEQ ID NO:1, and the peptide is defined by residues 22-64 of SEQ ID NO:2. The carboxyl end of lunasin contains a chromatin-binding domain, a cell adhesion motif Arg-Gly-Asp (RGD)

followed by eight Asp residues (Galvez and de Lumen, 1997; Galvez and de Lumen, 1999). The chromatin-binding domain consists of a 10-amino acid helical region homologous to a short conserved region found in other chromatin binding proteins (Aasland and Stewart, 1995). Mammalian studies provide evidence that lunasin may play a role in the cell cycle control (Galvez and de Lumen, 1999; Galvez et al., 2001; Jeong et al., 2002). For example, transfection of the lunasin gene into mammalian cells results in mitotic arrest and subsequent cell death (Galvez and de Lumen, 1999). In addition, exogenous addition of chemically synthesized lunasin to mammalian cells demonstrates that lunasin colocalizes with hypoacetylated chromatin; preferentially binds deacetylated histone H4 *in vitro;* and prevents histone H3 and H4 acetylation *in vivo* in the presence of a histone deacetylase inhibitor (Galvez et al., 2001). Acetylation and deacetylation of conserved histone N-terminal tails result in chromatin conformational changes that induce or suppress gene expression. It has been hypothesized that Lunasin modulates changes in chromatin organization by modifying histone tails, thereby, affecting gene expression that leads to its anti-neoplastic properties. Recently, lunasin was isolated from barley and was reported to possess the same biological activity ascribed to chemically synthesized lunasin (Jeong et al., 2002).

[05] While transfection of a cell with lunasin leads to cell death, lunasin peptide has been shown to have anti-neoplastic properties (Galvez et al., 2001). Significant suppression of chemical carcinogen-induced, e.g. 7,12-dimethylbenz[a]-anthracene (DMBA) and 3-methylcholanthrene (MCA), foci formation in C3H 10T1/2 mouse embryo fibroblast cells was observed when lunasin was added exogenously at nanomolar concentrations. In addition, topical application of lunasin inhibited skin tumorigenesis in female SENCAR mice. Lunasin peptide has also been shown to induce apoptosis in E1A-transfected C3H10T1/2 cells (Galvez et al., 2001) and suppress foci formation in E1A-transfected mouse fibroblast NIH 3T3 cells (Lam, et al., in press). E1A is a viral onco-protein that inactivates the Rb (retinoblastoma) tumor suppressor (Nevins, 1992). Furthermore, when C3H 10T1/2 and MCF-7 human breast cancer cells were treated with lunasin in the presence of the histone deacetylase inhibitor, sodium butyrate, a 10- to 95-fold reduction in acetylation of core histones H3 and H4 was observed (Galvez et al.,

2001). The genome-wide reduction in core histone acetylation suggests an epigenetic mechanism of action for lunasin that can influence gene expression fundamental to carcinogenesis.

[06] Prostate cancer is the most common non-dermatological carcinoma in the United States with an estimated 220,900 new cases and 28,900 deaths in 2003 (ACS, 2003). This type of cancer is the second leading cause of death among American men (www.cancer.org). Effects of anticancer agents on gene expression profiles of prostate cell lines using cDNA microarray analysis have been reported (Kudoh et al., 2000; Li et al., 2003; Zembutsu et al., 2003).

BRIEF DESCRIPTION OF THE INVENTION

[07] The present invention encompasses gene expression profiles produced in response to lunasin exposure. Such gene expression profiles correlate with anti-neoplastic activity at a cellular level and can be used in methods for screening potential anti-neoplastic agents. Additionally, these gene expression profiles can be used in methods for treatment (both prophylactic and active) and in monitoring of a subject having a neoplastic disease or having a risk factor for a neoplastic disease. Additionally, the invention includes microarrays used to measure the expression of particular sets of genes.

[08] The invention encompasses a method for screening a test compound for anti-neoplastic activity, the method comprising: providing a cell, measuring expression by the cell of a plurality of genes selected from Table 1, exposing the cell to the test compound, and re-measuring the expression by the cell of the plurality of genes, wherein the degree of increase in expression of the plurality of genes corresponds to the degree of anti-neoplastic activity of the test compound. In certain embodiments, the degree of increase of gene expression of the plurality of genes is measured using a weighted average. This method may employ screening any number of genes selected from Table 1, for example, at least 10, 20, 50, 80, 100, 121 or 123 from Table 1may be screened. This method commonly employs an array (or "microarray) comprising a substrate and a plurality of polynucleotide probes affixed to the substrate. The array generally comprises a plurality

of polynucleotide probes that are specifically complementary to a plurality of genes as shown in Table 1.

[09] The invention also encompasses a method for treatment and monitoring of a subject having a neoplastic disease. The method comprises administering lunasin (or related or derived compounds) to the subject, and monitoring the change in expression levels of at least one gene selected from a set of genes known to be up-regulated by lunasin.

[10] The invention further encompasses a method for prophylactically treating and monitoring a subject having one of more cancer risk factors. The method comprises administering lunasin (or related or derived compounds) and monitoring expression levels of at least one gene selected from a set of genes known to be up-regulated by lunasin.

[11] The invention further encompasses a method for monitoring anti-neoplastic activity in cell culture or in a subject during treatment (reactive or prophylactic). The method comprises taking a baseline reading of gene expression for at least one gene selected from a set of genes known to be up-regulated by lunasin; administering lunasin (or a derived or related compound, or providing some other treatment to the subject or cell culture); and then re-measuring the expression of at least one of the genes being monitored. Such a method may be useful for research to determine the efficacy of various drugs.

[12] The invention also includes microarrays comprising a set of genes selected from the 123 genes shown in this disclosure to be up-regulated by lunasin by at least two-fold.

[13] The invention also includes methods for preventing neoplastic growth in an organism comprising administering an agent, wherein the agent up-regulates the activity or expression of at least one, two, three, four, five, six or more genes selected from the

123 genes shown in this disclosure to be up-regulated by lunasin by at least two-fold. The agent is generally lunasin or a related or derived compound.

SUMMARY OF THE FIGURES

[14] Figure 1 shows the real-time reverse transcription-polymerase chain reaction (rtPCR) analysis of selected genes in normal prostate epithelial cells (RWPE-1) and malignant prostate epithelial cells (RWPE-2) treated with 2 microMoles lunasin. HIFIA-hypoxia-inducible factor 1, alpha subunit; PRKARIA- protein kinase, cAMP-dependent, regulatory, type I, alpha; TOB1- transducer of ERBB2, 1; THSB1- thrombospondin 1

DETAILED DESCRIPTION OF THE INVENTION

[15] It is known that lunasin suppresses chemically-induced carcinogenesis in mammalian cells and suppresses skin tumor formation in mice. In the present disclosure microarray analysis was used to determine the changes in gene expression profiles of normal (RWPE-1) and malignant (RWPE-2) prostate epithelial cell lines after 24 hour exposure to synthetic lunasin. Results of the microarray experiments disclosed herein support the anti-neoplastic property of lunasin and help elucidate its molecular mechanism. Various genes found by this study to be up-regulated by lunasin are known to play a role in cell growth, differentiation and tumor suppression and other important physiological activity directly or indirectly related to neoplastic transformation. It is therefore reasoned that lunasin suppresses neoplastic transformation by up-regulating various genes. 123 such genes are disclosed in this study to be up-regulated in the presence of lunasin by greater than two-fold. Of these 123 genes, 121 genes were up-regulated in RPWE-1 normal cells and only 2 genes were up-regulated in RPWE-2 malignant epithelial cells after 24h exposure to the lunasin peptide.

[16] Monitoring the expression of these 123 genes can be employed in a number of methods useful in therapy, in drug screening and in research into anti-neoplastic compounds. Since many of these genes are tumor suppressors, are involved in apoptosis or have other anti-neoplastic functions, it can be reasoned that an increase in the expression of such genes indicates an increase in anti-neoplastic activity. If this increase

in expression occurs in response to the administration of a drug (such as lunasin) then the increase in expression can reasonably be used as a quantitative marker that correlates with the degree of anti-neoplastic effectiveness of the drug treatment. Thus methods involving measurement of gene expression can be used to monitor efficacy of treatment, and to predict likely clinical outcomes. In drug screening, an animal or cell culture is exposed to a compound, and the expression of one or a plurality of genes is monitored to screen putative drug candidates. The greater the average increase in gene expression of the genes in a particular panel (e.g., a panel of genes listed in Table 1 or Table 2), the higher the score of the drug candidate. Such prioritization is routinely used by drug discovery companies. Gene expression profiles may be produced using arrays (microarrays) and quantitatively scored by measuring the average increase in gene expression for a panel of genes in response to exposure to a set quantity of a compound for a set time. The score may be weighted by ascribing greater weight to specific genes. For example, a panel of genes may be selected to include the 121 genes were up-regulated in RPWE-1 in this study. Particular weight may be given to the genes that are known tumor-suppressors (e.g., PRKAR1A, PKA, TOB1, ERBB2IP, and ERBIN). Algorithms for scoring and weighting expression array results are well known in the art and one of skill could readily create or adapt an algorithm for use with the present methods.

[17] The invention encompasses a method for treatment and monitoring of a subject having a neoplastic disease. The method comprises administering lunasin (or related or derived compounds) to the subject, and monitoring the change in expression levels of at least one gene selected from a set of genes known to be up-regulated by lunasin. Clinical symptoms may simultaneously be monitored to measure disease progression and/or the efficacy of treatment before, during and after the administration of lunasin.

[18] By monitoring one or a plurality of the 123 up-regulated genes disclosed in this study before, during and after the administration of lunasin, efficacy of treatment may be monitored, and clinical outcomes can be better predicted. Such monitoring may be used to determine appropriate treatment and drug dosages.

[19] The invention further encompasses a method for prophylactically treating and monitoring a subject having one of more cancer risk factors. The method comprises administering lunasin (or related or derived compounds) and monitoring expression levels of at least one gene selected from a set of genes known to be up-regulated by lunasin.

[20] The invention further encompasses a method for monitoring anti-neoplastic activity in cell culture or in a subject during treatment. The method comprises taking a baseline reading of gene expression for at least one gene selected from a set of genes known to be up-regulated by lunasin; administering lunasin (or a derived or related compound, or providing some other treatment to the subject or cell culture); and then re-measuring the expression of at least one of the genes being monitored. Such a method may be useful for research to determine the efficacy of various drugs, combinations of drugs and formulations to treat or prevent neoplasia. Such drugs may include lunasin, optionally in combination with other neoplastic compounds and adjuvants.

[21] The invention also includes microarrays comprising a at least one or a plurality of genes selected from the 123 genes shown in this disclosure to be up-regulated by lunasin by at least two-fold (the term "plurality" is means two or more). In certain embodiments, the microarray may include all 123 genes, or may include only the 121 genes were up-regulated in RPWE-1 normal cells. Such a microarray may be employed in the above methods for monitoring the gene expression profile of a subject (or cell culture) treated lunasin (or a derived or related compound). By looking at changes in the gene expression profile, a qualitative and/or quantative assessment can be deduced as to the degree to which genes are up-regulated in response to a treatment, and therefore the effectiveness of a treatment may be determined.

[22] The invention further includes methods for screening compounds for anti-neoplastic activity using the arrays described herein. Such methods involve exposure of cultured cells, tissues, organs or whole animals to a test compound, and the measurement

of expression of a plurality of genes before and after exposure to the test compound. The microarray used may include any desired number of the 123 genes disclosed herein as being up-regulated in the presence of lunasin. For example the array may include 2, 10, 25, 55, 100, 121 or 123 such genes.

[23] Microarrays are well known in the art and consist of a plurality of polynucleotides arranged regularly on a substrate such as paper, nylon or other type of membrane, filter, gel, polymer, chip, glass slide, or any other suitable support. The polynucleotides on the substrate bind complementary polynucleotides in a sample, thereby forming a hybridization complex and allowing sensitive and accurate detection. The polynucleotides may be cDNAs of gene open reading frames (or parts of genes) that bind specifically to complimentary to mRNAs. Often the polynucleotides are short oligonucleotides of between about 6 and 25 bases in length. In some instances, the mRNAs of the sample may be used to create an amplified cDNA library (using PCR) and this library may then be screened using an array. In the present case, a microarray may include one or more polynucleotides or oligonucleotides derived from of the 123 genes shown in this disclosure to be up-regulated by lunasin by at least two-fold.

[24]

In the present disclosure, the term "polynucleotide" refers to an oligonucleotide, nucleotide, or polynucleotide, and fragments thereof, and to DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand.

[25]

The above methods may include exposure of a subject or cell culture, or ex-vivo or in vitro tissue or organ to lunasin or related or derived compounds. In the present disclosure "related or derived compounds" include variations of lunasin such as a lunasin peptide sequence altered by addition, deletion or substitution of one or more amino acid. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR Inc., Madison Wisconsin). Variant peptides of lunasin may have at least

97% amino acid sequence identity over 43 amino acids with the lunasin peptide. In other embodiments, the variant peptide may have different degrees of identity such as at least 95%, 90%, 85%, 80%, 75%, 70%, or 60% or less identity with lunasin. Variants can be made using any of a variety of methods well known in the art. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More rarely, a variant may have "nonconservative" changes, e.g., replacement of a glycine with a tryptophan. The changes can be made at any site in the lunasin sequence. Mutants may be screened for the optimal anti-neoplastic activity, revealed for example, by the microarray screening assay disclosed herein. Thus, a suitable variant is one which would activate at least particular genes of interest, such as PKA, TOB1, ERBIN, NIP3, TSP1, BUB1B, TTK, PSMC6, USP1 and the like, in normal cells, or would activate a minimum number of genes or markers, such as at least 25 genes or markers, at least 50 genes or markers, at least 75 genes or markers and so on, in a non-malignant cell.

[26] The invention also includes methods for preventing neoplastic growth in an organism, a cell, cell culture, tissue of organ comprising administering an agent, wherein the agent up-regulates the activity or expression of at least one, two, three, four, five, six or more genes selected from the 123 genes shown in this disclosure to be up-regulated by lunasin by at least two-fold. The agent is generally lunasin or a related or derived compound.

[27] In this study, normal (RPWE-1) and malignant (RWPE-2) prostate epithelial cells, were treated with chemically synthesized lunasin peptide for 24 hours. The effects of exogenous lunasin on the comprehensive gene expression profiles were examined using Affymetrix Human Genome U133A Arrays that can screen up to 22,215 genes. Results of the microarray analysis showed that a total of 123 genes had a greater than twofold change in expression. Of these genes, 121 genes were up-regulated in RPWE-1 normal cells and only 2 genes were up-regulated in RPWE-2 malignant epithelial cells after 24h exposure to the lunasin peptide. No genes were down-regulated in either cell line. Those

genes up-regulated in RPWE-1 cells include genes involved in the control of cell division, tumor suppression and cell death.

[28] The microarray data was validated by performing real-time reverse-transcription PCR on selected genes. It is proposed that lunasin prevents cancer in vitro by up-regulating the expression of genes that prevent the onset of the neoplastic disease. Lunasin appears to have little effect on cells already transformed. These results support previous findings suggesting that lunasin may be a powerful anti-neoplastic molecule, up-regulating genes involved in the suppression of neoplastic transformation.

[29] Lunasin, a soybean peptide, has been demonstrated to prevent cell transformation and foci formation induced either by chemical carcinogens and or by oncogene transformation of mammalian cells (Galvez et al., 2001). A previous study of genes affected by lunasin showed that the lunasin increased by five fold, the p21/WAF1/Cip1 protein levels in cell transfected by the E1A oncogene but not in untransfected control cells (Lam et al., in press). It was suggested that p21/WAF1/Cip1, a potent and universal inhibitor of cyclin-dependent kinases (Gartel et al., 1996; Gartel and Tyner, 1999), is the prime candidate gene regulated by lunasin. However, the mechanism for how lunasin affects p21/WAF1/Cip1 regulation was not established. In contrast, microarray results did not show up-regulation of p21/WAF1/Cip1 transcript. Instead, the gene SP3, a transcriptional activator of p21/WAF1/Cip1 (Sowa et al., 1999) was up-regulated.

[30] The molecular mechanism for how lunasin suppresses cell transformation is still unknown. A model to explain how lunasin suppresses E1A cell transformation has been proposed by Lam et al. (in press). The model proposes that in the presence of lunasin, inactivation of the Rb (retinoblastoma) by E1A dissociates the Rb-HDAC (histone deacetylase) complex and reveals deacetylated core histones. Lunasin competes with HAT in binding to the deacetylated core histones and keeps the chromatin in a condensed and transcriptionally inactive state. The cell perceives this condition as abnormal and commits itself to apoptosis.

[31] Besides the Western blot analysis of p21/WAF1/Cip1 protein levels, nothing was known before this study about what genes are regulated by lunasin. In this study, a microarray analysis was performed to determine the global gene expression profile of normal and malignant prostate epithelial cells after exogenous addition of lunasin peptide into the culture media. The microarray data revealed that lunasin up-regulates genes that are involved in mitotic check point, tumor suppressor genes and genes that are involved in apoptosis. This suggests that lunasin may be acting as a transcriptional activator that up-regulates genes that protect the cells from transformation. This interpretation is *contrary* to a previously proposed role of lunasin as a repressor of gene expression (Galvez et al., 2001). It is also interesting to note that lunasin does not have an effect on prostate epithelia cells that are already malignant. This finding agrees with previous experiments which show that lunasin does not appear to have an effect on a cell that is already transformed.

[32] Aside from lunasin, several other components of soybean have been proposed to act as anti-cancer agents (Kennedy, 1995). For example, the Bowman-Birk Inhibitor (BBI), a soybean derived serine protease has been shown to posses anti-carcinogenic activity in both *in vitro* and *in vivo* systems (Kennedy, 1998). However, in contrast to our results, BBI and BBI concentrate (BBIC), a soybean concentrate enriched in BBI, has no effect on normal prostate epithelial cells but inhibited the growth, invasion and clonogenic survival of prostate cancer cell lines (Kennedy and Wan, 2002). The precise mechanism(s) for the suppressive effects of BBI and BBIC is currently under investigation.

[33] Another possible anti-neoplastic agent from soy is genistein, a major isoflavone in soybeans. Genistein has been found to inhibit carcinogenesis both *in vitro* and *in vivo* (Barnes, 1995) and it is known to inhibit the activation of the nuclear transcription factor, NF-kappa-B and the Akt signaling pathway, both of which are known to maintain the balance between cell survival and apoptosis (Sarkar and Li, 2002). Evidence shows that genistein induces apoptosis by up-regulating Bax, a protein that antagonizes the anti-apoptotic function of Bcl-2 (Sarkar and Li, 2002). A recent study was performed to

examine the gene expression profiles of PC3 prostate cancer cells treated with genistein (Li and Sarkar, 2002; Li and Sarkar, 2002). Results of microarray analysis shows that genistein regulates the expression of genes that are involved in control of cell growth, cell cycle, apoptosis, cell signaling, angiogenesis, tumor cell invasion and metastasis (Li and Sarkar, 2002; Li and Sarkar, 2002).

[34] The study disclosed herein is the first to use gene expression profiling to investigate the potential anti-neoplastic properties of a peptide derived from soybean. Based on the data obtained from our microarray analysis, it is proposed that lunasin is a transcriptional activator that up-regulates genes necessary for guarding or protecting the cells from transformation events. The inventors reason that lunasin may prime the cell for apoptosis and up-regulate the expression of some tumor suppressor genes and genes involved in the activation of mitotic checkpoint. Furthermore, the selective effect of lunasin on human gene expression supports an extensive body of epidemiological data linking high soybean intake and reduced risks of certain types of cancer such as breast, prostate and colon (Messina et al., 1994).

Pharmaceutical compositions and Drug Delivery

[35] Lunasin, or variants and derivatives thereof can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the active ingredient and a pharmaceutically acceptable carrier. Methods of formulation and delivery of peptide drugs is well known in the art and will not be discussed here.

[36] Methods for preparation of such formulations will be apparent to those skilled in the art. The materials also can be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc.

[37] The instant invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) cancer.

[38] The invention now will be exemplified in part by the following non-limiting examples.

EXAMPLES

Cell culture and lunasin treatment.

[39] Rostate epithelial cells, RWPE-1 (normal) and RWPE-2 (malignant) were cultivated in the Keratinocyte-Serum free medium with 5ng/ml rEGF and 0.05 mg/ml bovine pituitary extract. Cells were grown to 70% confluence, after which, cells were harvested and transferred to a 150 mm^2 plate at a cell density of 1 x 10^7 cells/ml. Lunasin peptide was added to a final concentration of 2μM. The cells were incubated for 24 hours after lunasin treatment. Lunasin has been shown to localize in the nucleus after 18 hours of incubation (Yi et al. in press). RWPE-1 and RWPE-2 cells that were not treated with lunasin served as negative controls.

[40] ***Microarrray analysis.*** Total RNA from each treatment was isolated by Trizol (Invitrogen, Carlsbad, CA). The cDNA used in microarray analysis was synthesized from 10 μg of total RNA using the SuperScript Choice system (Invitrogen). The cDNA was then transcribed *in vitro* in the presence of biotin-labeled nucleotide triphophates using T7 RNA polymerase after phenol-chloroform extraction and ethanol precipitation. cRNA was purified using the RNeasy mini kit (Qiagen) and fragmented at 94°C for 30 min in the buffer containing 0.2 M Tris-acetate (pH 8.1) 0.5 M potassium acetate, and 0.15 M magnesium acetate. Fragmented cRNA was hybridized overnight at 45°C to the human genome U133A Genechips (Affymetrix) representing approximately 22,215 transcripts. Hybridization was then detected using a confocal laser scanner (Affymetrix). The gene expression levels of samples were normalized and analyzed using RMA analysis (Irizarry et al., 2003). RMA analysis has been shown to have a higher sensitivity and specificity than dCHIP (Li and Wong, 2001) or MAS 5.0 (Affymetrix, 1999). Average-linkage hierarchal clustering of data was applied using the Cluster (Eisen et al., 1998) and the results were displayed with TreeView (Eisen et al., 1998).

[41] ***Quantitative PCR.*** To confirm microarray data, the total RNA prepared for microarray analysis was used for RT-PCR analysis of selected genes. The cDNA used for quantitative PCR was synthesized from 3 μg of total RNA using the SuperScript First-Strand Synthesis for RT-PCR kit (Invitrogen), following manufacturer's recommendations. The cDNA was diluted 4-fold and 2μl of cDNA was added to the quantitative PCR reaction using FAM-labeled TaqMan probes purchased from Applied Biosystems. The quantitative PCR reactions were performed in triplicate using a PRISM® ABI 7900HT Sequence Detection System (Applied Biosystems) and the expression of the ß-actin gene (BACT) was used for normalization. Changes in expression were calculated using relative quantification as follows: $\Delta\Delta Ct = \Delta Ctq - \Delta Ctcb$; where Ct = the cycle number at which amplification rises above the background threshold, ΔCt = the change in Ct between two test samples, q = the target gene, and cb = the calibrator gene. Gene expression is then calculated as $2^{-\Delta\Delta Ct}$ (Applied Biosystems).

[42] ***Gene expression profiles.***
The gene expression profiles of normal (RWPE-1) and malignant (RWPE-2) cells treated with lunasin were assessed using microarray analysis. The results of this analysis indicated that of the 22,215 gene interrogated, 123 genes had a greater than twofold change in expression. Of these genes, 121 genes were up-regulated in RPWE-1 cells and only two genes were up-regulated in RPWE-2 cells. No genes were down-regulated in either normal or malignant epithelial cells. Genes that were up-regulated in RPWE-1 cells include genes that are involved in the control of cell division, tumor suppression and cell death (Tables 1 and 2).

[43] Target verification using RT-PCR
Changės in mRNA level detected by microarray analysis were confirmed using real-time RT-PCR analysis of four genes: thrombospondin 1(THBS1), protein kinase, cAMP-dependent , regulatory, type 1 alpha (PRKAR1A), transducer of ERBB2, 1 (TOB1) and hypoxia inducible factor 1, alpha subunit (HIF1A) . The results of the real-time RT-PCR analysis for these selected genes were consistent with the microarray data. These results support our interpretation of the microarray data; that lunasin up-regulates the expression

of genes of normal prostate epithelial cell but not in established malignant prostate epithelial cells.

[44] Lunasin upregulates genes for apoptosis

Transfection of lunasin into mammalian cells results in arrest of mitosis leading to apoptosis. The anti-mitotic effect of lunasin is attributed to the binding of its poly-aspartyl carboxyl end to regions of hypoacetylated chromatin, like that found in kinetochores in centromeres (Galvez and de Lumen, 1999). Apoptosis is thought to be triggered when the kinetochore complex does not form properly and the microtubules fail to attach to the centromeres that lead to mitotic arrest and eventually cell death. Results of the microarray analysis showed that exogenous addition of lunasin up-regulates certain genes that are known to have a direct or indirect role in the induction of apoptosis in cells. These genes include thrombospondin 1 (THBS1), BCL2/adenovirus E1B 19kDa interacting protein 3 (BNIP3), and protein kinase C-like 2 (PRKCL2). THBS1 (also called TSP-1) is a member of a family of extracellular proteins that participate in cell-to-cell and cell-to-matrix communication (Bornstein, 1995). The role of THBS1 in the process of apoptosis or programmed cell death in cancer cells has recently been reviewed (Friedl et al., 2002). THBS1 induces apoptosis by activating the caspase death pathway (Nor et al., 2000). In addition, THBS1 has also been shown to have a potent anti-angiogenic activity (Nor et al., 2000) and induction of apoptosis by THSB1 is associated with decreased expression of the anti-apoptotic protein, Bcl-2 (Nor et al., 2000). We find it intriguing that lunasin up-regulates the expression of BNIP3, a gene that inhibits the anti-apoptotic activities of Bcl-2. BNIP3, formerly known as Nip3, is a mitochondrial protein that activates apoptosis and overcomes Bcl-2 (anti-apoptotic protein), suppression of cell death (Chen et al., 1997; Chen et al., 1999; Ray et al., 2000). A more recent study shows that BNIP3 mediates a necrosis-like cell death independent of apoptotic events, such as release of cytochrome c, caspase activation and nuclear translocation of apoptosis-inducing factor (Velde et al., 2000). Evidence indicates that BNIP3 causes cell death through opening of the mitochondrial permeability transition pore resulting in mitochondrial dysfunction and plasma membrane damage. Another gene that is up-regulated by lunasin is the hypoxia-inducible factor-1α (HIF1-A), a basic-helix-loop-

helix transcription factor which regulates the expression of BNIP3 (Wang et al., 1995). The BNIP3 promoter contains a functional HIF-1-responsive element and is potently activated by both hypoxia and forced expression of HIF-1A (Bruick, 2000). Studies have also shown that HIF-1A binds and stabilizes p53, a tumor suppressor (An et al., 1998; Chen et al., 2003). On the other hand, PRKCL2, also termed PRK2, promotes apoptosis by inhibiting the anti-apoptotic activities of Akt, an oncogene (Koh et al., 2000). Akt exerts its anti-apoptotic effects by phosphorylation and thereby inactivating BAD, a pro-apoptotic Bcl-2 family protein (Khwaja, 1999). However, a PRKCL2 C-terminal fragment generated during the early stages of apoptosis binds Akt, resulting in the inhibition of the Akt-mediated phosphorylation of BAD, thereby allowing apoptosis to occur (Koh et al., 2000). Based on this microarray data, we propose that lunasin primes the cell for apoptosis, by upregulating genes that inhibit anti-apoptotic activities of Akt and some BCL2 members, e.g. BAD and BCL-2. We also suggest that lunasin may be indirectly involved in stabilization of tumor suppressor p53 via HIF1A.

[45] Lunasin up-regulates genes involved in suppression of cell proliferation

Lunasin inhibitory effects on cell growth can be explained by the up-regulation of genes that play a role in tumor-suppression or anti-proliferation. For example, lunasin up-regulates a tumor suppressor gene encoding the cyclic AMP-dependent protein kinase A type I-α regulatory subunit, PRKARIA, (Sandrini et al., 2002). Mutations in the PRKARIA results in the Carney complex (CNC), a multiple neoplasia syndrome that is associated with thyroid tumorigenesis (Sandrini et al., 2002; Stergiopoulos and Stratakis, 2003). It is proposed that *PRKARIA* mutant cells have de-regulated control of gene expression which results in the activation of pathways, e.g. cAMP signaling, that lead to abnormal growth and proliferation (Stergiopoulos and Stratakis, 2003). Another gene up-regulated by lunasin, BTB (POZ) containing domain 1 (ABTB1 or BPOZ) is thought to be as one of the mediators of the growth-suppressive signaling pathway of the tumor suppressor, PTEN (Unoki and Nakamura, 2001). Overexpression of BPOZ inhibited cell cycle progression and suppressed growth of cancer cells while the transfection of BPOZ anti-sense accelerates cell growth (Unoki and Nakamura, 2001). Tob (also referred to as Tob1) is up-regulated by lunasin and is a member of the anti-proliferative BTG/Tob

family (Sasajima et al., 2002). Mice that are Tob deficient are prone to spontaneous formation of tumors (Yoshida et al., 2003). Further experiments also show that Tob acts a transcriptional co-repressor and suppresses the cyclin D1 promoter activity through an interaction with histone deacetylase (Yoshida et al., 2003). Our microarray results however, do not show down regulation of cyclin D1. The gene, erbb2 interacting protein (ERBIN), a novel suppressor of Ras signaling is up-regulated by lunasin. Erbin, a leucine-rich repeat containing protein, interacts with Ras and interferes with the interaction between Ras and Raf resulting in the negative regulation of Ras-mediated activation of extra-cellular signal regulated kinases (Erk) (Huang et al., 2003). The Ras oncogene is one of the most common mutations occurring in about 30% of human cancers (Duursma and Agami, 2003). Mutations that cause constitutive activation of Ras results in a continuous signal that tells the cells to grow regardless of whether or not receptors on the cell surface are activated by growth factor (Macaluso et al., 2002).

[46] Lunasin upregulates mitotic check point genes

Other genes up-regulated by lunasin is include the mitotic checkpoint genes like budding uninhibited benzimidazoles 1 homolog beta (BUB1B or BubR1), TTK protein kinase (MPS1 yeast homolog) and mitotic arrest deficient 2-like 1 (MAD2L1). Mitotic spindle checkpoint proteins monitor proper microtubule attachment to chromosomes prior to progression through mitosis allowing correct segregation of chromosomes into progeny cells (Lengauer et al., 1998). TTK is a protein kinase that phosphorylates MAD1p, a phosphorylation essential to the activation of the mitotic checkpoint (Farr and Hoyt, 1998). In yeast, MPS1 is required early in the spindle assembly checkpoint (Hardwick et al., 1996). It is suggested to be a limiting step in checkpoint activation, since it can activate the pathway when over expressed. Overexpression of MPS1 is able to delay cell cycle progression into anaphase in a manner similar to check activation by spindle damage (Hardwick et al., 1996). MPS1 is also required of the essential process of spindle pole body duplication (Winey et al., 1991). BUBR1 is a protein kinase required for checkpoint control. Evidence shows that inactivation of BubR1 by microinjection of specific antibodies abolishes the checkpoint control (Chan et al., 1999). A study further revealed that endogenous BubR1 protein levels is decreased in some breast cancer cell

lines; furthermore, evidence show, an oncogenic protein, breast cancer-specific gene 1 (BCSG1) directly interact is BubR1 which allows the degradation of BubR1 though a proteosome machinery (Gupta et al., 2003). It is speculated that BSCG1-induced reduction of the BubR1 protein allow breast cancer to progress at least in part by compromising the mitotic check point control through the inactivation of BubR1 (Gupta et al., 2003). Another check point gene MAD2L1 was reported to have reduced expression in a human breast cancer cell line exhibiting chromosome instability and aneuploidy (Li and Benezra, 1996). Some breast cancer cell lines show a mutation in the MAD2L1 gene that creates a truncated protein product; however, the specific role of MAD2L1 in breast cancer is still under investigation (Percy et al., 2000). We propose that lunasin up-regulates these mitotic check point genes to allow a heightened level of molecular surveillance to prevent premature cell division, chromosome instability and aneuploidy.

[47] Lunasin upregulates genes involved in protein degradation

It is also interesting to note that lunasin up-regulates several genes involved in protein degradation and turnover via the ubiquitin pathway. These genes include the proteosome 26S subunit ATPase 6 (PSMC6); E3 ubiquitin ligase (SMURF2), ubiquitin specific protease 1 (USP1); and ubiquitin-activating enzyme E1C (UBE1C). It is possible that lunasin up-regulates these genes to mediate the degradation of proteins that are required for the onset of cell transformation and foci formation.

[48] Lunasin up-regulates the gap junction protein, connexin 43

Adjacent cells communicate with each other through gap junctional channels that allow the passage of small molecules (Loewenstein and Rose, 1992). This process is referred to as "gap junctional intercellular communication" (GJC) and it is blocked in many cancer cells, including malignant human prostate cells (Hossain et al., 1999). Gap junctional channels are composed of proteins called connexins (Bruzzone et al., 1996). Lunasin up-regulates the expression of a gap junction protein called connexin 43, which has been shown to have a tumor suppressive role. Decreased expression and impaired posttranslational modification of connexin43 was observed in several prostate tumor cell

lines but not in normal cells suggesting that the loss of junctional communication is a critical step in the progression to human prostate cancer (Hossain et al., 1999). Studies have shown that the viral oncogene Src disrupts cell growth regulation by adding a phosphate group to a tyrosine residue in connexin 43, thereby blocking gap junction communication (Kanemitsu et al., 1997). Transfection of a functional connexin 43 gene to tumorigenic mouse cells resulted in the restoration of GJC, normal growth regulation and cell-to-cell communication, as well as, suppression of tumorigenesis (Rose et al., 1993).

[49] Although the invention has been described with reference to various specific embodiments, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims and any accompanying amendments.

Table 1. Complete list of genes up-regulated in normal RWPE-1 epithelial cells (Section A) and in Tumorogenic prostate RWPE-2 epithelial cells (Section A), after 24 hour exposure to lunasin.

	Affymetrix probe sets	Gene identifiers	Gene Name (Note: EASE version 2.0 was used for annotation)	Official Gene Symbol
	A. Genes up-regulated in non-tumorigenic prostate epithelial cell line (RWPE-1)			
1	200914_x_at	3895	kinectin 1 (kinesin receptor)	KTN1
2	201730_s_at	7175	translocated promoter region (to activated MET oncogene)	TPR
3	200915_x_at	3895	kinectin 1 (kinesin receptor)	KTN1
4	213229_at	23405	Dicer1, Dcr-1 homolog (Drosophila)	DICER1
5	200050_at	7705	zinc finger protein 146	ZNF146
6	201667_at	2697	gap junction protein, alpha 1, 43kDa (connexin 43)	GJA1
7	201699_at	5706	proteasome (prosome, macropain) 26S subunit, ATPase, 6	PSMC6
8	204455_at	667	bullous pemphigoid antigen 1, 230/240kDa	BPAG1
9	208896_at	8886	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	DDX18
10	200603_at	5573	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A
11	212648_at	54505	DEAH (Asp-Glu-Ala-His) box polypeptide 29	DHX29
12	216268_s_at	182	jagged 1 (Alagille syndrome)	JAG1
13	218181_s_at	54912	hypothetical protein FLJ20373	
14	219918_s_at	259266	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	ASPM
15	203789_s_at	10512	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	SEMA3C
16	217975_at	51186	pp21 homolog	
17	204240_s_at	10592	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	SMC2L1
18	202169_s_at	60496	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT
19	214709_s_at	3895	kinectin 1 (kinesin receptor)	KTN1
20	221802_s_at	57698	KIAA1598 protein	
21	201713_s_at	5903	RAN binding protein 2	RANBP2
22	212629_s_at	5586	protein kinase C-like 2	PRKCL2
23	220085_at	3070	helicase, lymphoid-specific	HELLS
24	213168_at	6670	Sp3 transcription factor	SP3
25	212888_at	23405	Dicer1, Dcr-1 homolog (Drosophila)	DICER1
26	212245_at	90411	multiple coagulation factor deficiency 2	MCFD2
27	213294_at		hypothetical protein FLJ38348	
28	208808_s_at	3148	high-mobility group box 2	HMGB2
29	202704_at	10140	transducer of ERBB2, 1	TOB1
30	212582_at	114882	oxysterol binding protein-like 8	OSBPL8
31	202381_at	8754	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	ADAM9
32	212640_at		hypothetical protein LOC201562	
33	211953_s_at	3843	karyopherin (importin) beta 3	KPNB3
34	205596_s_at	64750	E3 ubiquitin ligase SMURF2	SMURF2
35	211929_at	10151	heterogeneous nuclear ribonucleoprotein A3	HNRPA3
36	201889_at	10447	family with sequence similarity 3, member C	FAM3C
37	203820_s_at	10643	IGF-II mRNA-binding protein 3	

38	208731_at	5862	RAB2, member RAS oncogene family	RAB2
39	211967_at	114908	pro-oncosis receptor inducing membrane injury gene	PORIMIN
40	217945_at	53339	BTB (POZ) domain containing 1	BTBD1
41	211257_x_at	27332	NP220 nuclear protein	
42	212250_at		LYRIC/3D3	
43	207941_s_at	9584	RNA-binding region (RNP1, RRM) containing 2	RNPC2
44	200605_s_at	5573	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A
45	201486_at	5955	reticulocalbin 2, EF-hand calcium binding domain	RCN2
46	217941_s_at	55914	erbb2 interacting protein	ERBB2IP
47	203755_at	701	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	BUB1B
48	201242_s_at	481	ATPase, Na+/K+ transporting, beta 1 polypeptide	ATP1B1
49	201737_s_at	10299	similar to S. cerevisiae SSM4	
50	221773_at	2004	ELK3, ETS-domain protein (SRF accessory protein 2)	ELK3
51	217816_s_at	57092	PEST-containing nuclear protein	
52	209187_at	1810	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	DR1
53	202760_s_at	11217	A kinase (PRKA) anchor protein 2	AKAP2
54	212352_s_at	10972	transmembrane trafficking protein	
55	213285_at	NA	hypothetical protein LOC161291	
56	212692_s_at	987	LPS-responsive vesicle trafficking, beach and anchor containing	LRBA
57	212718_at	27249	hypothetical protein CL25022	
58	209259_s_at	9126	chondroitin sulfate proteoglycan 6 (bamacan)	CSPG6
59	201595_s_at	55854	likely ortholog of mouse immediate early response, erythropoietin 4	
60	202551_s_at	51232	cysteine-rich motor neuron 1	CRIM1
61	218067_s_at	55082	hypothetical protein FLJ10154	
62	211945_s_at	3688	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	ITGB1
63	209025_s_at	10492	synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP
64	202599_s_at	8204	nuclear receptor interacting protein 1	NRIP1
65	201991_s_at	3799	kinesin family member 5B	KIF5B
66	202413_s_at	7398	ubiquitin specific protease 1	USP1
67	209422_at	51230	chromosome 20 open reading frame 104	C20orf104
68	201132_at	3188	heterogeneous nuclear ribonucleoprotein H2 (H')	HNRPH2
69	214055_x_at	23215	HBxAg transactivated protein 2	
70	203743_s_at	6996	thymine-DNA glycosylase	TDG
71	211969_at	3320	heat shock 90kDa protein 1, alpha	HSPCA
72	204059_s_at	4199	malic enzyme 1, NADP(+)-dependent, cytosolic	ME1
73	221505_at	81611	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	ANP32E
74	212408_at	26092	lamina-associated polypeptide 1B	
75	212615_at	80205	hypothetical protein FLJ12178	
76	218577_at	55631	hypothetical protein FLJ20331	
77	201735_s_at	1182	chloride channel 3	CLCN3
78	200995_at	10527	importin 7	IPO7
79	217758_s_at	56889	SM-11044 binding protein	
80	201505_at	3912	laminin, beta 1	LAMB1
81	201690_s_at	7163	tumor protein D52	TPD52
82	203362_s_at	4085	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1

83	202277_at	10558	serine palmitoyltransferase, long chain base subunit 1	SPTLC1
84	208783_s_at	4179	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	MCP
85	217523_at		Data not available	
86	204822_at	7272	TTK protein kinase	TTK
87	218542_at	55165	chromosome 10 open reading frame 3	C10orf3
88	201939_at	10769	serum-inducible kinase	
89	204976_s_at	9949	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	AMMECR1
90	202234_s_at	6566	solute carrier family 16 (monocarboxylic acid transporters), member 1	SLC16A1
91	204258_at	1105	chromodomain helicase DNA binding protein 1	CHD1
92	201862_s_at	9208	leucine rich repeat (in FLII) interacting protein 1	LRRFIP1
93	213070_at	6165	ribosomal protein L35a	RPL35A
94	204058_at	4199	malic enzyme 1, NADP(+)-dependent, cytosolic	ME1
95	201734_at		chloride channel 3	CLCN3
96	209272_at	4664	NGFI-A binding protein 1 (EGR1 binding protein 1)	NAB1
97	201745_at	5756	PTK9 protein tyrosine kinase 9	PTK9
98	213729_at	55660	formin binding protein 3	FNBP3
99	209115_at	9039	ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)	UBE1C
100	201849_at	664	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3
101	212455_at	91746	splicing factor YT521-B	
102	201689_s_at	7163	tumor protein D52	TPD52
103	201110_s_at	7057	thrombospondin 1	THBS1
104	212149_at	23167	KIAA0143 protein	
105	212192_at	115207	potassium channel tetramerisation domain containing 12	KCTD12
106	209476_at	81542	thioredoxin domain containing	TXNDC
107	214363_s_at	9782	matrin 3	MATR3
108	201567_s_at	2803	golgi autoantigen, golgin subfamily a, 4	GOLGA4
109	200626_s_at	9782	matrin 3	MATR3
110	203804_s_at	10414	acid-inducible phosphoprotein	
111	200977_s_at	8887	Tax1 (human T-cell leukemia virus type I) binding protein 1	TAX1BP1
112	212893_at	26009	zinc finger, ZZ domain containing 3	ZZZ3
113	201435_s_at	1977	eukaryotic translation initiation factor 4E	EIF4E
114	215548_s_at	23256	sec1 family domain containing 1	SCFD1
115	212248_at		LYRIC/3D3	
116	201398_s_at	23471	translocation associated membrane protein 1	TRAM1
117	201304_at	4698	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NDUFA5
118	203987_at	8323	frizzled homolog 6 (Drosophila)	FZD6
119	208925_at	56650	chromosome 3 open reading frame 4	C3orf4
120	204094_s_at	9819	KIAA0669 gene product	
121	200989_at	3091	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A

B. Genes up-regulated in tumorigenic prostate epithelial cell line (RWPE-2)

1	203325_s_at	1289	collagen, type V, alpha 1	COL5A1
2	201551_s_at	3916	lysosomal-associated membrane protein 1	LAMP1

Table 2. Partial list of genes up-regulated in normal epithelial cells (RWPE-1) after 24 hour exposure to 2 micromolar lunasin, organized by gene function.

	Unigene cluster	Gene ID	Symbol	Fold-change
a) Tumor suppressive (anti-proliferative) genes				
protein kinase, cAMP-dependent, regulatory, type I, alpha	Hs.280342	5573	PRKAR1A, PKA	2.45
transducer of ERBB2, 1	Hs.178137	10140	TOB1	2.32
erbb2 interacting protein	Hs.8117	55914	ERBB2IP, ERBIN	2.23
b) Genes involved in apoptosis				
protein kinase C-like 2	Hs.69171	5586	PRKCL2, PRK2	2.33
BCL2/adenovirus E1B 19kDa interacting prot. 3	Hs.79428	664	BNIP3, NIP3	2.05
thrombospondin 1	Hs.164226	7057	THBS1, TSP1	2.05
pro-oncosis receptor inducing membrane injury gene	Hs.172089	114908	PORIMIN	2.26
serine palmitoyltransferase, long chain base subunit 1	Hs.90458	10558	SPTLC1	2.12
c) Mitotic checkpoint control genes				
BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	Hs.36708	701	BUB1B, BUBR1	2.23
TTK protein kinase	Hs.169840	7272	TTK	2.08
MAD2 mitotic arrest deficient-like 1 (yeast)	Hs.79078	4085	MAD2L1	2.12
d) Protein degradation genes				
proteasome (prosome, macropain) 26S subunit, ATPase, 6	Hs.156171	5706	PSMC6	2.58
RAN binding protein 2	Hs.199179	5903	RANBP2	2.36
E3 ubiquitin ligase SMURF2	Hs.438968	64750	SMURF2	2.29
ubiquitin specific protease 1	Hs.35086	7398	USP1	2.23
ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)	Hs.154320	9039	UBE1C	2.15